



## SEQUENCE LISTING

110 Becker, Iris

Vlodavsky , Israel

Reinstein, Elena

5,170- POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

41305 01/22/81

4150: US 09,776,874

4151: 2001-02-06

&lt;150&gt; US09/158,892

4151: 1999-03-01

&lt; 150&gt; PCT/US98/17954

<151> 1998-08-31

<150> US 09,109,386

&lt;151&gt; 1998-07-02

<150> US 08,922,170

(151) 1997-09-02

**Figure 1**

© 1998 Parsoft in version 3.1

219 1

2115 27

12. 11A

<400> 1  
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<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

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<211> 23

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<210> 5

<211> 15

<212> DNA

<213> Artificial sequence

<220> <223> Synthetic oligonucleotide

<220>

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11

<210> 1

<211> 23

<212> DNA

<213> Artificial sequence

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<223> Synthetic oligonucleotide

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23

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gtagtgatgc catgtaactg aatc

24

<210> 8

<211> 9

<212> PRT

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<220>

<223> Peptide derived from tryptic digestion of human heparinase

<400> 9

Tyr Gly Pro Asp Val Gly Gln Pro Arg

1

9

<210> 9

<211> 1721

<212> DNA

|||||

|||||

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 aactggactt cttacccag gagccgctgc acctggtgag cccctcgttc ctgtccgtta 240  
 ccaattgacgc caactcgggc aggcacccgc ggttctctat cctctcggtt tctccaaagc 300  
 ttgtacctt ggccagaggc ttgtctctg cgtacctgag gtttgggtgg accaagacag 360  
 atttctaat ttctgaccc aagaaggaat caactttga agagagaagt taatggcaat 420  
 ttaagtcac ccaggatatt tgcacatag gacacatcc tcttgatgtg gagggagaagt 480  
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 caggactgga ctgaccttt ggctaaatg cgttattaaq aacacagat ttgagtgga 660  
 acagttctaa tgcctagttg ctctggact actgctcttc caaggggtat aacatttctt 720  
 gggaactagg caatgaacct aacagtttc ttaagaaggc tgatatttc atcaatgggt 780  
 cgcagttagg agaagattat attcaattgc ataatcttc aagaagtc ccctccccc 840  
 atgcaaaact ctatggtct gatgttggtc agcctogaag aaagacggct aagatgctga 900  
 agagcttctt gaaggtggt ggagaagtga ttgattcagt tacatggcat caactactt 960  
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 ggttaggaga aacaagctct gcataaggag gggagcgcc ctgctatcc gacacctttg 1140  
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 tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttc atgcacaaac 1380  
 ctgacaatcc aaggtataaa gaaggagatt taactctgta tgcataaac ctccataacg 1440  
 tcaccaagta ctgcggtta ccctatctt ttctaaaca gcaagtggat aaataccttc 1500  
 taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaac 1560  
 taaagatggt gcatcatca accttgcac cttaaatgga aaaaactct cggccaggaa 1620  
 attactta ctgcaccc ttctatata gttttttt gataagaa atcaagttg 1680  
 tttttttt tttttttt attttttt tttttttt 1740

(210) 10

(211) 543

(212) PRT

(213) Homo sapiens

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
 20 35 30  
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
 35 40 45  
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
 50 55 60  
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
 65 70 75 80  
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
 85 90 95  
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
 100 105 110  
 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
 115 120 125  
 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
 130 135 140  
 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
 145 150 155 160  
 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
 165 170 175  
 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
 180 185 190  
 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
 195 200 205  
 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
 210 215 220  
 His His Asn Ser Phe Leu Lys Lys Ala Asp His Phe Ile Asn Gly Ser  
 225 230 235 240  
 His Leu Gly His Arg Tyr Ile Val Leu His Lys Leu Leu Arg Lys Ser  
 245 250 255  
 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
 260 265 270  
 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Leu Ala Gly His His  
 275 280 285 290 295 300  
 Ala Thr Ala Ala Arg His Leu Asn His Asp Val Leu Arg His His His

305	310	315	320
Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly	325	330	335
Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala	340	345	350
Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys	355	360	365
Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val	370	375	380
Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro	385	390	395
Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr	405	410	415
Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg	420	425	430
Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly	435	440	445
Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu	450	455	460
Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu	465	470	475
Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn	485	490	495
Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met	500	505	510
Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Ile Ser	515	520	525
Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Lys Ile	530	535	540

• 219 • 11

• 111 • 1721

212 DNA

(13) *Homo sapiens*

120.

4221 • J. Neurosci., September 24, 2008 • 28(39):4215–4228

222 · (63) .. (1691)

223.

&lt;400&gt; 11

ctagagcttt cgaactctcc ctacgcgaca gctagcggag ggaacagcca ggtgagccca 60

ag atg ctg ctg cgc tgg aag cct gcg ctg cca cca cca ctg atg ctg 107

Met	Leu	Leu	Arg	Ser	Lys	Pro	Ala	Leu	Pro	Pro	Pro	Leu	Met	Leu
1				5					10					15

ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc ggt ggc ctg ccc cga 155

Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg  
20 25 30

cct gcg caa gca caq qac gtc gtg qac ctg qac ttc ttc acc caq qag 203

Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu  
35 40 45

ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc 251

Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala  
50 55 60

aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag 299

Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys  
65 70 75

ctt cgt acc ttg ggc aga ggc ttg tct cct ggc tac ctg agg ttt ggt 347

Leu	Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly
80					85				90						95

ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc 395

Gly	Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr
				100					105					110	

\*t\* aad iij aad aat tar \*ij aad tet aad qic aad aad iat att tar 445

Thr Glu Arg Ser Tyr Trp Gln Ser Asn Val Asn Gln Asp Ile Lys  
 115 120 125

ma' ta' tta' tta' at- qat qat ita qaq qaq aaq tta' qaq tta' haa

Lys Tyr Gly Ser Ile Pro Asp Val Glu His Lys Leu Arg Leu His  
130 135 140

tgj ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag 539

Tip Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys  
 145 150 155

11. The following table shows the number of people who attended the concert in each age group.

Phe Ile Asp Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr

Table 1. *Phylogenetic relationships of the studied species and their outgroups. The numbers in the parentheses indicate the number of individuals of each species. The numbers in the brackets indicate the number of individuals of each species that were used for the molecular analysis. The numbers in the brackets indicate the number of individuals of each species that were used for the morphological analysis. The numbers in the brackets indicate the number of individuals of each species that were used for the molecular analysis.*

195	200	205	
ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly 210 215 220			731
aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly 225 230 235			779
tgg cag tta gga gaa gat tat att gaa ttg cat aaa ctt cta aga aag Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys 240 245 250 255			827
tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro 260 265 270			875
aga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga Arg Arg Lys Thr Ala Lys Met Leu Ser Phe Leu Lys Ala Gly Gly 275 280 285			923
gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg 290 295 300			971
act gct acc agg gaa gat ttc cta aac cct gat gta ttg gac att ttt Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe 305 310 315			1019
att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro 320 325 330 335			1067
ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly 340 345 350			1115
ggc ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp 355 360 365			1163
aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln 370 375 380			1211
gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp 385 390 395			1259
cct tta cct gat tat tgg cta tct att cta ttc aag aaa tta gtg ggc Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Pro Lys Lys Leu Val Gly 400 405 410 415			1307
acc aat tta tta atc cca att tta cat att tta aat att att att att Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu 420 425 429			1355
aga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa aaa Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu 435 440 445			1403
ata tat tta act ctg tat pcc ata aac cta cat aac gta act aag tat Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr 450 455 460			1451

100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 429 435 440 445 450 455 460



aat ggt cta aet cta aag atg gtg gat gat caa acc ttg cca cct tta 1595  
 Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu  
 500 505 510

ata gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc 1643  
 Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe  
 515 520 525

cca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc 1691  
 Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
 530 535 540

tgaaaataaa atataactagt cctgacaactg 1721

<210> 12

<211> 824

<212> DNA

<213> Mus musculus

<400> 12

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tgggcataga agtcgtgatg aggcaggtgt tottcggagc aggcacactac cacttagtgg 180

atgaaaaatt tgagccttta cctgattact ggtctctctt totgttcaag aaactggtag 240

gtcccagggt gttactgtca agagtgaag gccagacag gagcaaacct cgagtgtatc 300

tcactgcac taactctat caccacagat atcaggaagg agatctaact ctgtatgtcc 360

tgaacctcca taatgtcacc aagcacttga aggtaccgcc tcggttggtc aggaacccag 420

tggatacgta ccttctgaag ccttcgggga cggatggatt actttccaaa totgtccaac 480

tgaacggtca aattctgaag atgggtgatg agcagacct gccagctttg acagaaaaac 540

ctctcccgga aggaagtga ctaagcctgc ctgccttttc ctatggtttt tttgtcataa 600

gaaatgccaa aatcgtctgt tgtatatgaa aataaaagga atacggtaac cctgagacaa 660

atccagggg ggtatatttt cctaaacaa aacttagtt taggagacca cctccttacc 720

acttctcga ctttcgggag ggtcggatcc acttcattat taacttcagt ctggtatttt 780

ctctcctggg actctctctt gttttacat ttatgga tttt 840

<210> 13

<211> 1899

<212> DNA

<213> Homo sapiens

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ctctcctggg actctctctt gttttacat ttatgga tttt 840

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 ctqggtcccc tctccctgg ccgcctgcgc cgaactgcgc aaqcaagga cgtcgtggac 360  
 ctgaactct tccacaaqa gccctgca cgtgtgagcc cctcgttct gtcgtcacc 420  
 attgaagcga acctggccac ggacccggc ttcctcctcc tctgggttc tccaaagctt 480  
 cgtaccttgg ccagaggctt gtctcctgg taactgaggt ttggtggac caagacagac 540  
 ttctaatct tgcctccaa gaagcaatca acctttgaag adagaagtta ctggaattct 600  
 caagtcaccc aggatatttg caaatatgga tccctccctc ctgatgttga ggagaagtta 660  
 cgtttggaat ggcctcacc ggagcaattg ctactccag aacactacca gaaaagttc 720  
 aagaacaga cctactcaag aagctctgta gatgtctat acacttttgc aaactgctca 780  
 ggaactgga ctgatctttg cctaaatgag ttattaagaa cagcagattt gcagtggaac 840  
 agttataatg ctacgttgt cctggactac tgccttccca aggggtataa cattctcttg 900  
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 accaagta ctgcqqtacc ctatcctttt tctaacaagc aactggataa atactttcta 1680  
 caactttta gactcattt attacttcc aactctatcc aattcattta tctactctc 1740  
 caattgttt atattcatt ctactcatt ttaattgaa cctctcttc gctcgaact 1800  
 tcaatgggt tccagcttt cctatataat tttttttga taagaattgc caaatttct 1860  
 atttccatct gaaaataaaa tataatagtc ctgacactg 1920

210-14

211-19

212-14

Met Glu Gly Ala Val Gly Gly Val Arg Arg Arg Asn Gly Ala Glu Glu  
 1 5 10 15  
 Arg Arg Lys Gly Arg Trp Gly Ser Ala Gly Gly Ser Ala Arg Ala Leu  
 20 25 30  
 Asp Ser Pro Leu Arg Gly Ser Trp Arg Gly Glu Gln Pro Gly Glu Pro  
 35 40 45  
 Lys Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu  
 50 55 60  
 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg  
 65 70 75 80  
 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu  
 85 90 95  
 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala  
 100 105 110  
 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys  
 115 120 125  
 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly  
 130 135 140  
 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr  
 145 150 155 160  
 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys  
 165 170 175  
 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu  
 180 185 190  
 Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys  
 195 200 205  
 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr  
 210 215 220  
 Phe Ala Asn Tyr Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu  
 225 230 235 240  
 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu  
 245 250 255  
 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Thr Gln Leu Thr  
 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

290                      295                      300  
 Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro  
 305                      310                      315                      320  
 Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly  
 325                      330                      335  
 Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg  
 340                      345                      350  
 Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe  
 355                      360                      365  
 Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro  
 370                      375                      380  
 Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly  
 385                      390                      395                      400  
 Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp  
 405                      410                      415  
 Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln  
 420                      425                      430  
 Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp  
 435                      440                      445  
 Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly  
 450                      455                      460  
 Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu  
 465                      470                      475                      480  
 Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu  
 485                      490                      495  
 Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr  
 500                      505                      510  
 Leu Arg Leu Ile Tyr His Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu  
 515                      520                      525  
 Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu  
 530                      535                      540  
 Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu  
 545                      550                      555                      560

1899

212 DNA

· 213 · Homo sapiens

220.

• 221 •

222 (94) . . (1869)

2232

gqgaagcga gcaaggaagt aqqaqaaac cggcagggc ggggggggtt ggattggag 60

cagtgaggagg gatgcagaag aggagtgagg ggg atg gag ggc gca gtg gga ggg 114  
Met Glu Gly Ala Val Gly Gly  
1 5

gtg agg agg cgt aac ggg gcg gag gaa agg aga aaa ggg cgc tgg ggc 162  
Val Arg Arg Arg Asn Gly Ala Glu Glu Arg Arg Lys Gly Arg Trp Gly  
10 15 20

tgg ggg gga gga agt gct aga gct ctc gac tct cgg ctg ggc ggc agc 210  
 Ser Ala Gly Gly Ser Ala Arg Ala Leu Asp Ser Pro Leu Arg Gly Ser  
 25 30 35

tgg cgg ggg gag cag cca ggt gag ccc aag atg ctg ctg cgc tgg aag 258  
 Trp Arg Gly Glu Gln Pro Gly Glu Pro Lys Met Leu Leu Arg Ser Lys  
 40 45 50 55

det ggg ctg cgg ccg atg atg ctg ctg etc ctg ggg cgg ctg ggt      306  
 Pro Ala Leu Pro Pro Leu Met Leu Leu Leu Leu Gly Pro Leu Gly  
                 60                 65                 70

ccc ctc tcc cct gcc ctg ccc cga cct gcg caa gca cag gac gtc 354  
Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro Ala Gln Ala Gln Asp Val  
75 30 85

gtg gac ctg gac ttc ttc acc cag gag ccg ctg cac ctg gtg age ccc 402  
Val Asp Leu Asp Phe Phe Thr Gln Glu Pro Leu His Leu Val Ser Pro  
6 25 30

For the city-to-city case: Att: GAG, PEE, AAC; Ctl: GAG, ACG, GAC; Ser: GAG, AAA  
 For the loop case: Val: Thr, Ile, Asp, Ala, Asn, Leu, Ala, Thr, Asp, Pro, Arg

Phe etc etc etc etc ggt tct cca aag att cgt acc ttg gcc aga ggc 498  
Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr Leu Ala Arg Gly  
126 125 130 135

119 ttt cgt gca tac atg arg ttt gat ggc acc aag aca gac ttc cta 546  
 Leu Ser Phe Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu  
 146 145 150

gat gtg gag gag aag tta cgg ttg gaa tgg ccc tac cag gag caa ttg Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln Glu Gln Leu 185 190 195	696
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*Ulaganathan, Vigneshwara, Jagadeeswarar, Aravamudan, Senthil Kumar* 1439

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35 40 45

Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala Thr Asp Pro Arg Phe Leu  
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Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser  
65 70 75 80

Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe  
85 90 95

Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser  
100 105 110

Gln Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val  
115 120 125

Leu Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu  
130 135 140

Arg Gln Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser  
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Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr  
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Ala His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu  
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Leu His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr  
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Ser Asp Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys  
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Val Thr Lys Glu Ile Thr Pro Gly Lys Lys Val Trp Leu Gly Glu Thr  
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340 345 350

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Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His  
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Leu Val Asp Glu Asn Phe Glu Pro Leu Pro Asp Tyr Trp Leu Ser Leu  
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Leu Phe Lys Lys Leu Val Gly Pro Arg Val Leu Leu Ser Arg Val Lys  
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Gly Pro Asp Arg Ser Lys Leu Arg Val Tyr Leu His Cys Thr Asn Val  
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Tyr His Pro Arg Tyr Gln Glu Gly Asp Leu Thr Leu Tyr Val Leu Asn  
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Leu Ser Lys Ser Val Gln Leu Asn Gly Gln Ile Leu Lys Met Val Asp  
 485 490 495

Glu Gln Thr Leu Pro Ala Leu Thr Glu Lys Pro Leu Pro Ala Gly Ser  
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Phe Leu Gly Ser Pro Arg Leu Arg Ala Leu Ala Arg Gly Leu Ser Pro	70	75	80	
aca tac ttg aga ttt ggc ggc aca aag act gac ttc ctt att ttt gat				884
Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp	85	90	95	
cgg gac aag gaa ccg act tcc gaa gaa aga agt tac tgg aaa tct caa				932
Pro Asp Lys Glu Pro Thr Ser Glu Glu Arg Ser Tyr Trp Lys Ser Gln	100	105	110	
gtc aac cat gat att tgg agg tct gag ccg gtc tct gct ggc ggc ttg				980
Val Asn His Asp Ile Cys Arg Ser Glu Pro Val Ser Ala Ala Val Leu	115	120	125	
agg aaa ctc cag gtg gaa tgg ccc ttc cag gag ctg ttg ctg ctc cga				1028
Arg Lys Leu Gln Val Glu Trp Pro Phe Gln Glu Leu Leu Leu Leu Arg	130	135	140	145
gag cag tac caa aag gag ttc aag aac agc acc tac tca aga agc tca				1076
Glu Gln Tyr Gln Lys Glu Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser	150	155	160	
gtg gac atg ctc tac agt ttt gcc aag tgc tgg ggg tta gac ctg atc				1124
Val Asp Met Leu Tyr Ser Phe Ala Lys Cys Ser Gly Leu Asp Leu Ile	165	170	175	
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Phe Gly Leu Asn Ala Leu Leu Arg Thr Pro Asp Leu Arg Trp Asn Ser	180	185	190	
tcc aac gcc cag ctt ctc ctt gac tac tgc tct tcc aag ggt tat aac				1220
Ser Asn Ala Gln Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn	195	200	205	
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cac att ctc atc gat ggg ttg cag tta gga gaa gac ttt gtg gag ttg				1316
His Ile Leu Ile Asp Gly Leu Gln Leu Gly Glu Asp Phe Val Glu Leu	230	235	240	
cat aaa ctt cta caa agg tca gct ttc caa aat gca aaa ctc tat ggt				1364
His Lys Leu Leu Gln Arg Ser Ala Phe Gln Asn Ala Lys Leu Tyr Gly	245	250	255	
cct gac atc ggt cag cct cga ggg aag aca ggt aaa ctg ctg aag agt				1412
Pro Asp Ile Gly Gln Pro Arg Gly Lys Thr Val Lys Leu Leu Arg Ser	260	265	270	
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Leu Leu Lys Ala Gln Gly Glu Val Ile Asp Ser Leu Thr Trp His His	275	280	285	
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Tyr Tyr Leu Asn Gly Arg Ile Ala Thr Lys Glu Asp Phe Leu Ser Ser	290	295	300	305
gat ggc ctg gac act ttt att ctc tct gtc caa aaa att ctg aag gtc				1556
Arg Ala Leu Asp Thr Phe Ile Leu Ser Val Gln Lys Ile Leu Lys Val	310	315	320	

[illegible]

• 210 • 36.

4211、 385

· 212 · ENA

(212) PATTUS NERVOSUS



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